

<110> GENSET S.A.

<120> NOVEL KCNQ POLYPEPTIDES, MODULATORS THEREOF, AND
THEIR USES IN THE TREATMENT OF MENTAL DISORDERS

<130> 794 WO

<150> US 60/391,359

<151> 2002-06-25

<160> 47

<170> PatentIn version 3.1

<210> 1

<211> 1932

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1932)

<223>

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Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
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gac tcc acc cgg gac ggg gcg ctg ctg atc gcc ggc tcc gag gcc ccc 144
Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
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aag cgc ggc agc atc ctc agc aaa cct cgc gcg ggc ggc gcg ggc gcc 192
Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
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Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
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ctc tac aac gtg ctg gag cgg ccg cgc ggc tgg gcg ttc atc tac cac 288
Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
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gcc tac gtg ttc ctc ctg gtt ttc tcc tgc ctc gtg ctg tct gtg ttt 336
 Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
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ctg gaa atc gtg act atc gtg gtg ttt ggc gtg gag tac ttc gtg cgg 432
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 Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
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gcc aca tct gcg ctc cgg agc ctg cgc ttc ctg cag att ctg cgg atg 624
 Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
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atc cgc atg gac cgg cgg gga ggc acc tgg aag ctg ctg ggc tct gtg 672
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gag aac gac cac ttt gac acc tac gcg gat gca ctc tgg tgg ggc ctg 816
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 Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
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Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
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ttc gcg ctg cct gca ggc atc ttg ggg tct ggg ttt gcc ctg aag gtt 960
Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
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cag gag cag cac agg cag aag cac ttt gag aag agg cgg aac ccg gca 1008
Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
325 330 335

gca ggc ctg atc cag tcg gcc tgg aga ttc tac gcc acc aac ctc tcg 1056
Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
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cgc aca gac ctg cac tcc acg tgg cag tac tac gag cga acg gtc acc 1104
Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
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Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu
370 375 380

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Lys Gly Ser Pro Cys Arg Gly Pro Leu Cys Gly Cys Cys Pro Gly Arg
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Arg Ser Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser Pro Ser Lys Val
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ccc aag agc tgg agc ttc ggg gac cgc agc cgg gca cgc cag gct ttc 1488
Pro Lys Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala Arg Gln Ala Phe
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cgc atc aag ggt gcc gcg tca cgg cag aac tca gaa gaa gca agc etc 1536
 Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu Glu Ala Ser Leu
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acc gag gac ctg acc ccg ggc ctc aaa gtc agc atc aga gcc gtg tgt 1632
 Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile Arg Ala Val Cys
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ccc tac gac gtg atg gac gtc atc gag cag tac tca gcc ggc cac ctg 1728
 Pro Tyr Asp Val Met Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu
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 Asp Met Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg Gln Glu Pro Arg
 580 585 590

ctg cct gtc cag cag ggg aca aga acg ggg tgg gct tct ggg aca aag 1824
 Leu Pro Val Gln Gln Gly Thr Arg Thr Gly Trp Ala Ser Gly Thr Lys
 595 600 605

ccc act gtg gcc cat ggt ggg agt gca ggg ggt gtg tgg gcg ggg cct 1872
 Pro Thr Val Ala His Gly Gly Ser Ala Gly Gly Val Trp Ala Gly Pro
 610 615 620

cct ccc cac cca cgt cgg cct ctg tca gct tct gtt gtg tct tca caa 1920
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Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
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Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
65 70 75 80

Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
85 90 95

Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
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Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
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Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
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Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
180 185 190

Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
195 200 205

Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
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Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
225 230 235 240

Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
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Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
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Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
275 280 285

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Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
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Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
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Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
340 345 350

Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
355 360 365

Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu
370 375 380

Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu Arg Asn Leu Lys Ser Lys
385 390 395 400

Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro Pro Glu Pro Ser Pro Ser

Lys Gly Ser Pro Cys Arg Gly Pro Leu Cys Gly Cys Cys Pro Gly Arg
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Ser Ser Gln Lys Val Ser Leu Lys Asp Arg Val Phe Ser Ser Pro Arg
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Gly Val Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala Gln Thr Val Arg
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485 490 495

Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu Glu Ala Ser Leu
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Pro Gly Glu Asp Ile Val Asp Asp Lys Ser Cys Pro Cys Glu Phe Val
515 520 525

Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile Arg Ala Val Cys
530 535 540

Val Met Arg Phe Leu Val Ser Lys Arg Lys Phe Lys Glu Ser Leu Arg
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Pro Tyr Asp Val Met Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu
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Asp Met Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg Gln Glu Pro Arg
580 585 590

Leu Pro Val Gln Gln Gly Thr Arg Thr Gly Trp Ala Ser Gly Thr Lys
595 600 605

Pro Thr Val Ala His Gly Gly Ser Ala Gly Gly Val Trp Ala Gly Pro
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Pro Pro His Pro Arg Arg Pro Leu Ser Ala Ser Val Val Ser Ser Gln
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Ser Leu Phe

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 Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
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gac tcc acc cgg gac ggg gcg ctg ctg atc gcc ggc tcc gag gcc ccc 144
 Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
 35 40 45

aag cgc ggc agc atc ctc agc aaa cct cgc gcg ggc ggc gcg gcc 192
 Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
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ggg aag ccc ccc aag cgc aac gcc ttc tac cgc aag ctg cag aat ttc 240
 Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
 65 70 75 80

ctc tac aac gtg ctg gag cgg ccg cgc ggc tgg gcg ttc atc tac cac 288
 Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
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gcc tac gtg ttc ctc ctg gtt ttc tcc tgc ctc gtg ctg tct gtg ttt 336
 Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe

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 Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
 145 150 155 160

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 195 200 205

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 225 230 235 240

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 245 250 255

gag aac gac cac ttt gac acc tac gcg gat gca ctc tgg tgg ggc ctg 816
 Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
 260 265 270

atc acg ctg acc acc att ggc tac ggg gac aag tac ccc cag acc tgg 864
 Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
 275 280 285

aac ggc agg ctc ctt gcg gca acc ttc acc ctc atc ggt gtc tcc ttc 912
 Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
 290 295 300

ttc gcg ctg cct gca ggc atc ttg ggg tct ggg ttt gcc ctg aag gtt 960
 Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
 305 310 315 320

cag gag cag cac agg cag aag cac ttt gag aag agg cgg aac ccg gca 1008
 Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
 325 330 335

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 Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
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cgc aca gac ctg cac tcc acg tgg cag tac tac gag cga acg gtc acc 1104
 Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
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gtg ccc atg tac agt tcg caa act caa acc tac ggg gcc tcc aga ctt 1152
 Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu
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 385 390 395 400

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 Gln Lys Val Ser Leu Lys Asp Arg Val Phe Ser Ser Pro Arg Gly Val
 420 425 430

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 Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu Glu Ala Ser Leu Pro Gly
 485 490 495

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 Glu Asp Ile Val Asp Asp Lys Ser Cys Pro Cys Glu Phe Val Thr Glu

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 Asp Leu Thr Pro Gly Leu Lys Val Ser Ile Arg Ala Val Cys Val Met
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gac gtg atg gac gtc atc gag cag tac tca gcc ggc cac ctg gac atg 1680
 Asp Val Met Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met
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ctg tcc cga att aag agc ctg cag tcc agg caa gag ccc cgc ctg cct 1728
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gtc cag cag ggg aca aga acg ggg tgg gct tct ggg aca aag ccc act 1776
 Val Gln Gln Gly Thr Arg Thr Gly Trp Ala Ser Gly Thr Lys Pro Thr
 580 585 590

gtg gcc cat ggt ggg agt gca ggg ggt gtg tgg gcg ggg cct cct ccc 1824
 Val Ala His Gly Gly Ser Ala Gly Gly Val Trp Ala Gly Pro Pro Pro
 595 600 605

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Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
50 55 60

Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
65 70 75 80

Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
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Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
100 105 110

Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
115 120 125

Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
130 135 140

Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
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Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
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Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
180 185 190

Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
195 200 205

Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
210 215 220

Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
225 230 235 240
12/150

Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
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Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
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Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
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Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
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Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
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Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
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Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu
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Gln Lys Val Ser Leu Lys Asp Arg Val Phe Ser Ser Pro Arg Gly Val
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Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser Pro Ser Lys Val Pro Lys
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465 470 475 480

Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu Glu Ala Ser Leu Pro Gly
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Glu Asp Ile Val Asp Asp Lys Ser Cys Pro Cys Glu Phe Val Thr Glu
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Asp Leu Thr Pro Gly Leu Lys Val Ser Ile Arg Ala Val Cys Val Met
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Val Gln Gln Gly Thr Arg Thr Gly Trp Ala Ser Gly Thr Lys Pro Thr
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Phe
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gac tcc acc cgg gac ggg gcg ctg ctg atc gcc ggc tcc gag gcc ccc 144
 Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
 35 40 45

aag cgc ggc agc atc ctc agc aaa cct cgc gcg ggc ggc gcg ggc gcc 192
 Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
 50 55 60

ggg aag ccc ccc aag cgc aac gcc ttc tac cgc aag ctg cag aat ttc 240
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 65 70 75 80

ctc tac aac gtg ctg gag cgg ccg cgc ggc tgg gcg ttc atc tac cac 288
 Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
 85 90 95

gcc tac gtg ttc ctc ctg gtt ttc tcc tgc ctc gtg ctg tct gtg ttt 336
 Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
 100 105 110

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 Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
 115 120 125

ctg gaa atc gtg act atc gtg gtg ttt ggc gtg gag tac ttc gtg cgg 432
 Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
 130 135 140

atc tgg gcc gca ggc tgc tgc tgc cgg tac cgt ggc tgg agg ggg cgg 480

Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
 145 150 155 160

ctc aag ttt gcc cgg aaa ccg ttc tgt gtg att gac atc atg gtg ctc 528
 Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
 165 170 175

atc gcc tcc att gcg gtg ctg gcc gcc ggc tcc cag ggc aac gtc ttt 576
 Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
 180 185 190

gcc aca tct gcg ctc cgg agc ctg cgc ttc ctg cag att ctg cgg atg 624
 Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
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gag aac gac cac ttt gac acc tac gcg gat gca ctc tgg tgg ggc ctg 816
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 Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
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Lys Gly Ser Pro Cys Arg Gly Pro Leu Cys Gly Cys Cys Pro Gly Arg
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Val Asn Ile Tyr Met Gln Arg Met Gly Ile Pro Pro Thr Glu Thr Glu
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Ala Tyr Phe Gly Ala Lys Glu Pro Glu Pro Ala Pro Pro Tyr His Ser
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Asp Thr Ser Ile Ser Ile Pro Ser Val Asp His Glu Glu Leu Glu Arg
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Leu Asn Ser Cys Tyr Ala Ala Val Ala Pro Cys Ala Lys Val Arg Pro
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Tyr Ile Ala Glu Gly Glu Ser Asp Thr Asp Ser Asp Leu Cys Thr Pro
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130

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Ile Asn Ser Ile Ser Val Asn Ser Asp Cys Glu Thr Tyr Met Ser Ala

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cccaccag c gtc atc atg acc ggg gcc tac aac aac ttc ttc cgc atg 151355
Val Ile Met Thr Gly Ala Tyr Asn Asn Phe Phe Arg Met
355 360

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Phe Asp Arg Asn Thr Lys Arg Asp Val Thr Leu Glu Ala Ser Arg Glu
365 370 375 380

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Ser Ser Lys Pro Arg Ala Val Leu Lys Pro Arg Arg Val Cys Val Gly
385 390 395

ggc aag cgc cgg cgt gat gac atc agt gtg gac agc ttg gac ttc acc 151499
Gly Lys Arg Arg Arg Asp Asp Ile Ser Val Asp Ser Leu Asp Phe Thr
400 405 410

aag aag atc ctg cac acg gcc tgg cac ccg gct gag aac atc att gcc 151547
Lys Lys Ile Leu His Thr Ala Trp His Pro Ala Glu Asn Ile Ile Ala
415 420 425

atc gcc gcc acc aac aac ctg tac atc ttc cag gac aag gta aac tct 151595
Ile Ala Ala Thr Asn Asn Leu Tyr Ile Phe Gln Asp Lys Val Asn Ser
430 435 440

gac atg cac tag g tatgtgcagt tcccggcccc tgccaccag cctcatgcaa 151648
Asp Met His
445

gtcatccccg acatgacctt cacgaccgca atgcaaggag gggaagaaag tcacagcact 151708

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<213> Homo sapiens

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Asn His Thr Gly Glu Leu Leu Ala Thr Gly Asp Lys Gly Gly Arg Val
35 40 45

Val Ile Phe Gln Arg Glu Pro Glu Ser Lys Asn Ala Pro His Ser Gln
50 55 60

Gly Asp Tyr Asp Val Tyr Ser Thr Phe Gln Ser His Glu Pro Glu Phe
65 70 75 80

Asp Tyr Leu Lys Ser Leu Glu Ile Glu Glu Lys Ile Asn Lys Ile Lys
85 90 95

Trp Leu Pro Gln Gln Asn Ala Ala His Ser Leu Leu Ser Thr Asn Asp
100 105 110

Lys Thr Ile Lys Leu Trp Lys Ile Thr Glu Arg Asp Lys Arg Pro Glu
115 120 125

Gly Tyr Asn Leu Lys Asp Glu Glu Gly Lys Leu Lys Asp Leu Ser Thr
130 135 140

Val Thr Ser Leu Gln Val Pro Val Leu Lys Pro Met Asp Leu Met Val
145 150 155 160

Glu Val Ser Pro Arg Arg Ile Phe Ala Asn Gly His Thr Tyr His Ile
165 170 175

Asn Ser Ile Ser Val Asn Ser Asp Cys Glu Thr Tyr Met Ser Ala Asp
180 185 190

Asp Leu Arg Ile Asn Leu Trp His Leu Ala Ile Thr Asp Arg Ser Phe
195 200 205

Asn Ile Val Asp Ile Lys Pro Ala Asn Met Glu Asp Leu Thr Glu Val
210 215 220

Ile Thr Ala Ser Glu Phe His Pro His His Cys Asn Leu Phe Val Tyr
225 230 235 240

Ser Ser Ser Lys Gly Ser Leu Arg Leu Cys Asp Met Pro Ala Ala Ala
245 250 255

Leu Cys Asp Lys His Ser Lys Leu Phe Glu Glu Pro Glu Asp Pro Ser
260 265 270

Asn Arg Ser Phe Phe Ser Glu Ile Ile Ser Ser Val Ser Asp Val Lys
275 280 285

Phe Ser His Ser Asp Arg Tyr Met Leu Thr Arg Asp Tyr Leu Thr Val
290 295 300

Lys Val Trp Asp Leu Asn Met Glu Ala Arg Pro Ile Glu Thr Tyr Gln
305 310 315 320

Val His Asp Tyr Leu Arg Ser Lys Leu Cys Ser Leu Tyr Glu Asn Asp
325 330 335

Cys Ile Phe Asp Lys Phe Glu Cys Ala Trp Asn Gly Ser Asp Ser Val
340 345 350

Ile Met Thr Gly Ala Tyr Asn Asn Phe Phe Arg Met Phe Asp Arg Asn
355 360 365

Thr Lys Arg Asp Val Thr Leu Glu Ala Ser Arg Glu Ser Ser Lys Pro
370 375 380

Arg Ala Val Leu Lys Pro Arg Arg Val Cys Val Gly Gly Lys Arg Arg
385 390 395 400

Arg Asp Asp Ile Ser Val Asp Ser Leu Asp Phe Thr Lys Lys Ile Leu
405 410 415

His Thr Ala Trp His Pro Ala Glu Asn Ile Ile Ala Ile Ala Ala Thr
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<222> (301)..(301)

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tgccgggtctc caccggcccc acgggcaccg tgccaatgcc tgcagagggg aggggggtgtg 180

aggggaaggt ggggcccagag gggatgctgg ggcaggatat tcggggacag agcctggaaa 240

ccaacaaagc ctgggactgg atcccccca caggcctggg ggttggggcc acatgggcgg 300

rgtcagggg aaggaggcc agggacaagg gcagacacag agattccaag ggaagtgggg 360

gctctccac ccagctgggg aaataagagg ctgagcagca gagctcccag gaaccacgg 420

aaaagccaca gggacagaga agcgggagga tgggcagaga ggggctgtct gaacctgggg 480

tccatcctt gccccggag agcacttcc ctcaaaggag gcactatggg accctcctt 540

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601

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<211> 601

<212> DNA

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<220>

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<220>

<221> allele

<222> (301)..(301)

<223> biallelic marker 30-2/62

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tgtgtggggg cagggggccct gctgacttag aaacaagtgg cacattgatc cgcattcaaa 180
cttgccagcc aatcaaccac agccccgcgc acagactctc ccagggtggga ctgaggggggt 240
ctccccgtc cttggcaggg ggtctcccc cagcaccgcc cagtccgct ctctccacag 300
rctccagatg cccacatccc cagaacactc aatgggacaa ctgagagcag gttacagaga 360
aagaaaagcc acacaagctc accaagggca cgctatttca gaagtgcctt ctctctctgg 420
aaatgtcgac cccaaagctc tcactgggaa acctctggcc tggccccggg aagcgacagg 480
cgcaggtttg gggctgaggc cgtcccagca gctctgtggc ctgccagacc tcagagcact 540
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gccagggtcg gtggcagggc tggcacaggg gaaccaggag gcgccgctgg cttcaccatc 180
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cgggggctga ccctgcca ttctgcagac aaagccacca ccctgccagg gctcaagagg 480
gaagaaaatg gggagggggc catttgagca aatgagcca cccgtgagca aggtggaggg 540
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cgtgcccatg ggggccaggg gtgctcagag tcttggtgct gtgggtgcct ctgtccaac 180
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ccaggggagc acatgggcac aggtcagcg ggactcctgg aatgttctct ctttctccac 300
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 tgagctggaa ctgttgacca ggacacacac atggccatgt ggctctggg ctctctcaca 240
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 ccccgggccc aaggggagga aatggagacc ccacctcca gtggaggga ggcaaggtcc 420
 cactgtgggg gtagcacatg ggatacacc atgtggctgc cgctggagac gtagtttgc 480
 cacaccgtt tctctacgt gaacatttgc ctgcatctca ccttctaact cctgggtgct 540
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<400> 47

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cagggcccac caggggctca caggaaaggt cgtggaaaat tacaagaaat ctccctctg 180
gcactagcgg gtgaggggaa tggaagccac cgccagacag caccatctcc tcacctctt 240
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a

601